

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle

(ii) TITLE OF INVENTION: Apomixis Conferred By Expression of SERK
Interacting Proteins

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Syngenta Patent Dept.
- (B) STREET: 3054 Cornwallis Road
- (C) CITY: RTP
- (D) STATE: NC
- (E) COUNTRY: USA
- (F) ZIP: 27709

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/EP99/07972
- (B) FILING DATE: 20-OCT-1999
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Meigs, J. Timothy
- (B) REGISTRATION NUMBER: 38,241
- (C) REFERENCE/DOCKET NUMBER: S-30683A

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 919-541-8587

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ACGTGTCCGT GGAGGCGGGT CGGGTCAGTC GGGTCAGATA CCAAGGTGCC AAGTGGAAAGG	60
TITGTGGGATG GATCTAACCA ATGCAAAGG TTATTACTCG AGACACCGAG TTTGTGGAGT	120
GCACACTAAA ACACCTAAAG TCACTGTGGC TGGTATCGAA CAGAGGTTT GTCAACAGTG	180
CAGCAGGTTT CATCAGCTTC CGGAATTGTA CCTAGAGAAA AGGAGITGCC GCAGGAGACT	240
CGCTGGTCAT AATGAGCGAC GAAGGAAGCC ACAGCCTGCG TCTCTCTCTG TGTTAGCTTC	300
TCGTTACGGG AGGATCGCAC CTTCGCTTTA CGAAAATGGT GATGCTGGAA TGAATGGAAG	360
CTTTCTTGGG AACCAAGAGA TAGGATGGCC AAGTCAAGA ACATTGGATA CAAGAGTGAT	420
GAGGCGGCCA GTGTCAATCAC CGTCATGGCA GATCAATCCA ATGAATGTAT TTAGTCAAGG	480
TTCAGTTGGT GGAGGAAGGA CAAGCTTCTC ATCTCCAGAG ATTATGGACA CTAAACTAGA	540
GAGCTACAAG G	551

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Glu	Met	Gly	Ser	Asn	Ser	Gly	Pro	Gly	His	Gly	Pro	Gly	Gln	Ala
1								10						15	

Glu	Ser	Gly	Gly	Ser	Ser	Thr	Glu	Ser	Ser	Ser	Phe	Ser	Gly	Gly	Leu
				20				25						30	

Met	Phe	Gly	Gln	Lys	Ile	Tyr	Phe	Glu	Asp	Gly	Gly	Gly	Ser	Gly	
					35			40				45			

Ser	Ser	Ser	Ser	Gly	Gly	Arg	Ser	Asn	Arg	Arg	Val	Arg	Gly	Gly	
					50			55			60				

Ser	Gly	Gln	Ser	Gly	Gln	Ile	Pro	Arg	Cys	Gln	Val	Glu	Gly	Cys	Gly
					65		70			75			80		

Met	Asp	Leu	Thr	Asn	Ala	Lys	Gly	Tyr	Tyr	Ser	Arg	His	Arg	Val	Cys
					85			90			95				

Gly	Val	His	Ser	Lys	Thr	Pro	Lys	Val	Thr	Val	Ala	Gly	Ile	Glu	Gln
					100			105			110				

Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Gln	Leu	Pro	Glu	Phe	Asp
					115			120			125				

Leu	Glu	Lys	Arg	Ser	Cys	Arg	Arg	Leu	Ala	Gly	His	Asn	Glu	Arg	
					130			135			140				

Arg	Arg	Lys	Pro	Gln	Pro	Ala	Ser	Leu	Ser	Val	Leu	Ala	Ser	Arg	Tyr
					145		150			155			160		

Gly	Arg	Ile	Ala	Pro	Ser	Leu	Tyr	Glu	Asn	Gly	Asp	Ala	Gly	Met	Asn
					165			170			175				

Gly	Ser	Phe	Leu	Gly	Asn	Gln	Glu	Ile	Gly	Trp	Pro	Ser	Ser	Arg	Thr
					180			185			190				

Leu	Asp	Thr	Arg	Val	Met	Arg	Arg	Pro	Val	Ser	Ser	Pro	Ser	Trp	Gln
					195			200			205				

Ile	Asn	Pro	Met	Asn	Val	Phe	Ser	Gln	Gly	Ser	Val	Gly	Gly	Arg	
					210		215			220					

Thr	Ser	Phe	Ser	Ser	Pro	Glu	Ile	Met	Asp	Thr	Lys	Leu	Glu	Ser	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225	230	235	240
Lys Gly Ile Gly Asp Ser Asn Cys Ala Leu Ser Leu Leu Ser Asn Pro			
245		250	255
His Gln Pro His Asp Asn			
260	265	270	
Asn Asn Asn Thr Trp Arg Ala Ser Ser Gly Phe Gly Pro Met Thr Val			
275	280	285	
Thr Met Ala Gln Pro Pro Pro Ala Pro Ser Gln His Gln Tyr Leu Asn			
290	295	300	
Pro Pro Trp Val Phe Lys Asp Asn Asp Asn Asp Met Ser Pro Val Leu			
305	310	315	320
Asn Leu Gly Arg Tyr Thr Glu Pro Asp Asn Cys Gln Ile Ser Ser Gly			
325	330	335	
Thr Ala Met Gly Glu Phe Glu Leu Ser Asp His His Gln Ser Arg			
340	345	350	
Arg Gln Tyr Met Glu Asp Glu Asn Thr Arg Ala Tyr Asp Ser Ser Ser			
355	360	365	
His His Thr Asn Trp Ser Leu			
370	375		

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 859 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (v) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
- (vi) IMMEDIATE SOURCE:
 - (B) CLONE: 3B39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCAACATTGC	TTCTTAACCA	GAAATCCACC	ATCATCTTCC	CACGAATACA	ACITAAAGCT	60
TTACCAGAAA	ATGGAGGGTC	AGAGAACACA	ACGCCGGGTT	TACTTGAAAG	ACAAGGCTAC	120
AGTCTCCAAC	CTTGTGAAAG	AAGAAATGGA	GAATGGCATG	GATGGAGAAG	AGGAGGATGG	180
AGGAGACGAA	GACAAAAGGA	AGAAGGTGAT	GGAAAGAGTT	AGAGGTCTTA	GCACTGACCG	240
TGTTCCATCG	CGACTGTGCC	AGGTGATAG	GTGCACTGTT	AATTGACTG	AGGCCAAGCA	300
GTATTACCGC	AGACACAGAG	TATGTGAACT	ACATGCAAAG	GCATCTGCTG	CGACTGTGTC	360
AGGGGTCAGG	CAACGCCCTTT	GTCAACAAATG	CAGCAGGTTT	CATGAGCTAC	CAGAGTTGA	420
TGAAGCTAAA	AGAAGCTGCA	GGAGGCGCTT	AGCTGGACAC	AATGAGAGGA	GGAGGAAGAT	480
CTCTGGTGAC	AGTTTGGAG	AAGGGTCAGG	CCGGAGAGGG	TTTACCGGTC	AACTGATCCA	540
GACTCAAGAA	AGAAACAGGG	TAGACAGGAA	ACTTCCTATG	ACCAACTCAT	CATTTAAGGG	600
ACCACAGATC	AGATAAACCC	TCCCGCTCTC	TCTCTCTGTT	CATCTACATA	TGCTCTATCT	660
ACACTCTTAT	TAGACAAATA	ATGGCATCTA	ACAATGTCAA	AAAAAGTTGG	TCATGGTATT	720
AAATCCTAGA	GGGAAATATA	AGTATAAACCC	TTTAGTCCCC	TTTATGCTGT	CCTGTAATGA	780
ATATCTATCC	GGAAATGTAT	TCGCATAGTC	TTGGCTCTAA	TAATGTTTAT	AAAAAAAAAA	840
AAAAAAAAAA	AAAAAAAAAA					859

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3B39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Glu	Gly	Gln	Arg	Thr	Gln	Arg	Arg	Gly	Tyr	Leu	Lys	Asp	Lys	Ala
1															15
5															

Thr	Val	Ser	Asn	Leu	Val	Glu	Glu	Met	Glu	Asn	Gly	Met	Asp	Gly
20														30

Glu	Glu	Glu	Asp	Gly	Gly	Asp	Glu	Asp	Lys	Arg	Lys	Lys	Val	Met	Glu
35															

Arg	Val	Arg	Gly	Pro	Ser	Thr	Asp	Arg	Val	Pro	Ser	Arg	Leu	Cys	Gln
50															

Val	Asp	Arg	Cys	Thr	Val	Asn	Leu	Thr	Glu	Ala	Lys	Gln	Tyr	Tyr	Arg
65															

Arg	His	Arg	Val	Cys	Glu	Val	His	Ala	Lys	Ala	Ser	Ala	Ala	Thr	Val
85															

Ala	Gly	Val	Arg	Gln	Arg	Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Glu
100															

Leu	Pro	Glu	Phe	Asp	Glu	Ala	Lys	Arg	Ser	Cys	Arg	Arg	Arg	Leu	Ala
115															

Gly	His	Asn	Glu	Arg	Arg	Lys	Ile	Ser	Gly	Asp	Ser	Phe	Gly	Glu
130														

Gly	Ser	Gly	Arg	Arg	Gly	Phe	Ser	Gly	Gln	Leu	Ile	Gln	Thr	Gln	Glu
145															

Arg	Asn	Arg	Val	Asp	Arg	Lys	Leu	Pro	Met	Thr	Asn	Ser	Ser	Phe	Lys
165															

Gly	Pro	Gln	Ile	Arg
180				

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGAACGAGAA AGGTAAAGCT ACAAGTAGTA GTGGAGTTG TCAGGTCGAG AGTTGTACCG	60
CGGATATGAG CAAAGCCAAA CAGTACCACA AACGACACAA AGTCTGCCAG TTTCATGCCA	120
AAGCTCCTCA TGITCGGATC TCTGGTCITC ACCAACGTTT CTGCCAACAA TGCAGCAGGT	180
TTCACCGCGCT CAGTGAGTTT GATGAAGCCA AGCGGAGTTG CAGGAGACGC TTAGCTGGAC	240
ACAACGAGAG AAGGCGGAAA AGCACAACTG ACTAAAGACG GTGAAACGTG TGAGATCCCG	300
GTTTGAAGGT TAATGAAACA GGCTTIGCTT ACTCTCTCTCT GTCACTCTCT TTTAGCTCCT	360
TGTAATCCCTC TGIGTCTCTG TCTGTTCTC CATATTACCT GIAATCAAAG CTATCTGCTA	420
AACCTACGAC ATGGTTAAAT AAATGCATTG AGACTTAAAA AAAAAAAAAA AAAAAAAAAA	479

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Met Arg Arg Ser Lys Ala Glu Gly Lys Arg Ser Leu Arg Glu
1 5 10 15

Leu Ser Glu Glu Glu Glu Glu Glu Thr Glu Asp Glu Asp Thr
20 25 30

Phe Glu Glu Glu Ala Leu Glu Lys Lys Gln Lys Gly Lys Ala Thr
35 40 45

Ser Ser Ser Gly Val Cys Gln Val Glu Ser Cys Thr Ala Asp Met Ser
50 55 60

Lys Ala Lys Gln Tyr His Lys Arg His Lys Val Cys Gln Phe His Ala
65 70 75 80

Lys Ala Pro His Val Arg Ile Ser Gly Leu His Gln Arg Phe Cys Gln
85 90 95

Gln Cys Ser Arg Phe His Ala Leu Ser Glu Phe Asp Glu Ala Lys Arg
100 105 110

Ser Cys Arg Arg Arg Leu Ala Gly His Asn Glu Arg Arg Arg Lys Ser
115 120 125

Thr Thr Asp
130

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2682 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

(B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGCATTCAAG GAGACACTAA TGGTGCTCTT ACITTTGAATC TTAATGGTGA AAGTGTGTC	60
CTTTTTCCCTG CCAAGAACAC CAAATCCGGA GCCGTTTGTC AGGTGAAAAA CTGTGAAAGCT	120
GATCTTAGTA AAGTTAAGGA TTATCATAGA CGCCATAAGG TCTGTGAGAT GCATTCCAAG	180
GCTACTAGTGT CCACTGTGCG AGGTATCTTG CAGGGCTTTT GTCAAGCAATG TAGTAGGTT	240
CATCTCTGC CAGGTTTCGA TGACGGAAAG AGAACGTTGTC GTAGACGTTT GGCTGGCCAT	300
AATAAACGTC CGAGGAAAAC AAATCCCGAA CCTGGCGCTA ACGGGAAATCC TAGTGTGATGAT	360
CACTCAAGCA ACTATCTCTT GATTACTCTC TTGAAGATAC TCTCCAATAT GCATAACCAT	420
ACCGGTGATC AAGATTGAT GTCTCATCTT CTGAAGAGCC TCGTAAGCCA TGCTGGCGAA	480
CAGTTAGGGA AAAACTTAGT TGAACCTCTT CTACAAGGAG AGATCTCAAG GTTCCTTAAA	540
ATATTGGAAA ACTCGGCCTT GCTTGGGATT GAGCAAGCTC CTCAAGAGGA GTAAAGCAA	600
TTTTOGGCTC GGCAAGATGG GACAGCTACC GAGAACAGAT CAGAAAAACA AGTCAAAATG	660
AATGATTTTG ATTTGAATGA TATCTATATA GACTCAGATG ACACAGACGT CGAAAGATCT	720
CCTCCTCCAA CGAATCCAGC GACCAGITCT CTTGATTATC CTTCATGGAT ACATCAGTCT	780
AGTCGGCCTC AGACAAGTAG GAATTCAAGAT TCAGCATCTG ACCAGTCACC CTCAAGITCT	840
AGTGAAGATG CTCAGATGCG CACAGGCCGG ATTGTGTC AACTATTGG GAAAGAGCCA	900
AATGAATTTC CTATTGTCCTT ACGAGGACAG ATTCTTGACT GGTTATCGCA TAGTCCAATC	960
GACATGGAGA GCTACATAAG ACCTGGCTGT ATCGTATTGA CCATCTATCT TCGTCAAGCT	1020
GAAACTGCTT GGGAAAGAACT TTCAGACGAT CTGGGTTTTA GCTTAGGGAA GCTTCTAGAT	1080
CTCTCCGATG ATCCCTTGIG GACAACCTGGA TGGATTATG TAGGGTGCAG AACCAACTTG	1140
CATTGTATA TAACGGTCAG GTTGTGTTG ACACITCAATT GTCTCTAAA AGTCGGTGT	1200
ATAGTCACAT CATTAGCGTT AAACCGCTTG CTATAGCTGC AACGGAGAAG GCTCAATTAA	1260

CAGTTAAAGG CATGAATCTC CGTCGGCGTG GCACAAGGTT ACITTTGTCT GTTGAAGGAA	1320
AATACTTGAT TCAGGAAACA ACACACGATT CGACGCCAG GGAGGGATGAC GATTCAAGG	1380
ACAACAGTGA GATTGTTGAG TGTTGAAACT TCTCTTGIGA TATGCCTATA TTGAGTGGTC	1440
GAGGATTCAT GGAGATTGAA GACCAAGGAC TCAGTAGCAG CTTCTCCCT TTCTTAGTGG	1500
TTGAAGATGA CGATGTTTGT TCTGAAATCC GTATACTTGA AACCACATTA GAGTCACTG	1560
GAACTGATTTC TGCTAACCAA GCTATGGATT TCATACATGA AATCGGTTGG CTTCTTCACA	1620
GAAGTAAACT TGGGGAAATCA GACCCAAATC CAGGGTTTT CCCATTAATA CGCTTCCAGT	1680
GGCTAACATCGA GTTCTCAATG GATCGAGAGT GGTGGCGTGT GATCAGAAAG CTATTAACAA	1740
TGTTCTTGA TGGAGCTGTT GGTGAATTTC CTTCCCTCCTC TAATGCCACA CTGTCAGAAC	1800
TGTGCCTTCT TCACAGAGCC GTGAGGAAAA ACTCTAACGCC TATGGTTGAA ATGCTCTTGA	1860
GATATATTCC CAAGCAACAG AGAAACAGCT TGTTTAGACC CGATGCTGCT GGTCCAGCCG	1920
GCTTAACACC TCTTCATAATT GCAGCTGGTA AAGACGGITC AGAAGATGTG TTGGATGCGC	1980
TAACAGAAGA TCCTGCAATG GTGGGGATTG AAGCGTGGAA GACATGTGCA GACAGCACAG	2040
GCTTCACACC AGAAGACTAC GCACGCTTAC GCGGTCACTT CTCATACATC CACTGATTG	2100
AACGCAAGAT CAATAAAAAG TCAACAACTG AAGATCAITG TGTTGTCAC ACATGGTTT	2160
CTTTCTCAGA CAGAGAGCAG AAAGAACCAA AATCAGGTCC GATGGCTTCA GCCTTGGAGA	2220
TCACACAGAT TCCATGCAAG CTCTGTGACC ATAAACTGGT GTATGGACA ACACCGAGGT	2280
CTGTAGCGTA CAGACCAGCT AIGTTGTCAA TGGTGGCGAT TGCTGCGGT TGCGTCTGTG	2340
TGGCACTTCT GTTTAAGAGT TGCCCGGAAG TGCTCTATGT GTTCAACCG TTCAGGTGGG	2400
AGITATTGGA CTATGGAACA AGCTGAGTGT AAGTCTACIT TGAAAGATCT TCTAAGATAT	2460
ATATATGAAT GTTACTTATA TAAAACCATA GAGGTGTGAT TTCTATATGT AACTATATGA	2520
GTATAAGATA TAGAGACATG TTGGAGAAGA AGATTGTGTT TATTATTGTT GTTGTGTG	2580
TTGTGTAAAAA GCCTCTCCTA TCTCTCTCGA ACCTAAGGAT TCTCTCTCTG ATTAGTATAT	2640
TTTTTGTGTTG ACAAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA	2682

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 848 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 3A52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Glü	Ala	Arg	Ile	Asp	Glu	Gly	Gly	Glu	Ala	Gln	Gln	Phe	Tyr	Gly
1															
															15

Ser	Val	Gly	Asn	Ser	Ser	Asn	Ser	Ser	Ser	Cys	Ser	Asp	Glu	Gly	
20															30

Asn	Asp	Lys	Lys	Arg	Arg	Ala	Val	Ala	Ile	Gln	Gly	Asp	Thr	Asn	Gly
35															45

Ala	Leu	Thr	Leu	Asn	Leu	Asn	Gly	Glu	Ser	Asp	Gly	Leu	Phe	Pro	Ala
50															60

Lys	Lys	Thr	Lys	Ser	Gly	Ala	Val	Cys	Gln	Val	Glu	Asn	Cys	Glu	Ala
65															80

Asp	Leu	Ser	Lys	Val	Lys	Asp	Tyr	His	Arg	Arg	His	Lys	Val	Cys	Glu
85															95

Met	His	Ser	Lys	Ala	Thr	Ser	Ala	Thr	Val	Gly	Gly	Ile	Leu	Gln	Arg
100															110

Phe	Cys	Gln	Gln	Cys	Ser	Arg	Phe	His	Leu	Leu	Pro	Gly	Phe	Asp	Asp
115															125

Gly	Lys	Arg	Ser	Cys	Arg	Arg	Leu	Ala	Gly	His	Asn	Lys	Arg	Pro	
130															140

Arg Lys Thr Asn Pro Glu Pro Gly Ala Asn Gly Asn Pro Ser Asp Asp
 145 150 155 160
 His Ser Ser Asn Tyr Leu Leu Ile Thr Leu Leu Lys Ile Leu Ser Asn
 165 170 175
 Met His Asn His Thr Gly Asp Gln Asp Leu Met Ser His Leu Leu Lys
 180 185 190
 Ser Leu Val Ser His Ala Gly Glu Gln Leu Gly Lys Asn Leu Val Glu
 195 200 205
 Leu Leu Leu Gln Gly Arg Arg Ser Gln Gly Ser Leu Asn Ile Gly Asn
 210 215 220
 Ser Ala Leu Leu Gly Ile Glu Gln Ala Pro Gln Glu Glu Leu Lys Gln
 225 230 235 240
 Phe Ser Ala Arg Gln Asp Gly Thr Ala Thr Glu Asn Arg Ser Glu Lys
 245 250 255
 Gln Val Lys Met Asn Asp Phe Asp Leu Asn Asp Ile Tyr Ile Asp Ser
 260 265 270
 Asp Asp Thr Asp Val Glu Arg Ser Pro Pro Pro Thr Asn Pro Ala Thr
 275 280 285
 Ser Ser Leu Asp Tyr Pro Ser Trp Ile His Gln Ser Ser Pro Pro Gln
 290 295 300
 Thr Ser Arg Asn Ser Asp Ser Ala Ser Asp Gln Ser Pro Ser Ser Ser
 305 310 315 320
 Ser Glu Asp Ala Gln Met Arg Thr Gly Arg Ile Val Phe Lys Leu Phe
 325 330 335
 Gly Lys Glu Pro Asn Glu Phe Pro Ile Val Leu Arg Gly Gln Ile Leu
 340 345 350
 Asp Trp Leu Ser His Ser Pro Thr Asp Met Glu Ser Tyr Ile Arg Pro
 355 360 365
 Gly Cys Ile Val Leu Thr Ile Tyr Leu Arg Gln Ala Glu Thr Ala Trp
 370 375 380
 Glu Glu Leu Ser Asp Asp Leu Gly Phe Ser Leu Gly Lys Leu Leu Asp
 385 390 395 400

Leu Ser Asp Asp Pro Leu Trp Thr Thr Gly Trp Ile Tyr Val Arg Val
 405 410 415

Gln Asn Gln Leu Ala Phe Val Tyr Asn Gly Gln Val Val Val Asp Thr
 420 425 430

Ser Leu Ser Leu Lys Ser Arg Asp Tyr Ser His Ile Ile Ser Val Lys
 435 440 445

Pro Leu Ala Ile Ala Ala Thr Glu Lys Ala Gln Phe Thr Val Lys Gly
 450 455 460

Met Asn Leu Arg Arg Arg Gly Thr Arg Leu Leu Cys Ser Val Glu Gly
 465 470 475 480

Lys Tyr Leu Ile Gln Glu Thr Thr His Asp Ser Thr Thr Arg Glu Asp
 485 490 495

Asp Asp Phe Lys Asp Asn Ser Glu Ile Val Glu Cys Val Asn Phe Ser
 500 505 510

Cys Asp Met Pro Ile Leu Ser Gly Arg Gly Phe Met Glu Ile Glu Asp
 515 520 525

Gln Gly Leu Ser Ser Ser Phe Phe Pro Phe Leu Val Val Glu Asp Asp
 530 535 540

Asp Val Cys Ser Glu Ile Arg Ile Leu Glu Thr Thr Leu Glu Phe Thr
 545 550 555 560

Gly Thr Asp Ser Ala Lys Gln Ala Met Asp Phe Ile His Glu Ile Gly
 565 570 575

Trp Leu Leu His Arg Ser Lys Leu Gly Glu Ser Asp Pro Asn Pro Gly
 580 585 590

Val Phe Pro Leu Ile Arg Phe Gln Trp Leu Ile Glu Phe Ser Met Asp
 595 600 605

Arg Glu Trp Cys Ala Val Ile Arg Lys Leu Leu Asn Met Phe Phe Asp
 610 615 620

Gly Ala Val Gly Glu Phe Ser Ser Ser Asn Ala Thr Leu Ser Glu
 625 630 635 640

Leu Cys Leu Leu His Arg Ala Val Arg Lys Asn Ser Lys Pro Met Val
 645 650 655

Glu Met Leu Leu Arg Tyr Ile Pro Lys Gln Gln Arg Asn Ser Leu Phe

	660	665	670
Arg Pro Asp Ala Ala Gly Pro Ala Gly Leu Thr Pro Leu His Ile Ala			
675	680	685	
Ala Gly Lys Asp Gly Ser Glu Asp Val Leu Asp Ala Leu Thr Glu Asp			
690	695	700	
Pro Ala Met Val Gly Ile Glu Ala Trp Lys Thr Cys Arg Asp Ser Thr			
705	710	715	720
Gly Phe Thr Pro Glu Asp Tyr Ala Arg Leu Arg Gly His Phe Ser Tyr			
725	730	735	
Ile His Leu Ile Gln Arg Lys Ile Asn Lys Lys Ser Thr Thr Glu Asp			
740	745	750	
His Val Val Val Asn Ile Pro Val Ser Phe Ser Asp Arg Glu Gln Lys			
755	760	765	
Glu Pro Lys Ser Gly Pro Met Ala Ser Ala Leu Glu Ile Thr Gln Ile			
770	775	780	
Pro Cys Lys Leu Cys Asp His Lys Leu Val Tyr Gly Thr Thr Arg Arg			
785	790	795	800
Ser Val Ala Tyr Arg Pro Ala Met Leu Ser Met Val Ala Ile Ala Ala			
805	810	815	
Val Cys Val Cys Val Ala Leu Leu Phe Lys Ser Cys Pro Glu Val Leu			
820	825	830	
Tyr Val Phe Gln Pro Phe Arg Trp Glu Leu Leu Asp Tyr Gly Thr Ser			
835	840	845	

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 576 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA to mRNA

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CAGCGGAAGA GCTCACCGIT GAAGAGAGGA ATCTCCTCTC TGTTGCCTAC AAAAACGTGA	60
TCGGATCTCT ACGCGCCGCC TGGAGGATCG TGTCTCGAT TGAGCAGAAG GAAGAGAGTA	120
GGAAGAACGA CGAGCACGTG TCGCTTGTCA AGGATTACAG ATCTAAAGTT GAGTCTGAGC	180
TTTCTTCTGT TTGCTCTGGA ATCCCTAAGC TCCTTGACTC GCATCTGATC CCATCTGCTG	240
GAGCGAGTGA GTCTAAGGTC TTTTACTTGA AGATGAAAGG TGATTATCAT CGGTACATGG	300
CTGAGTTTAA GTCTGGTGTAT GAGAGGAAAA CTGCTGCTGA AGATAACCATG CTCGCCTACA	360
AAGCAGCTCA GGATATCGCA GCTGCGGATA TGGCACCTAC TCATCCGATA AGGCTTGGTC	420
TGGCCCTGAA TTTCTCAGTG TTCTACTATG AGATTCTCAA TTCTTCAGAC AAAGCTTGTGTA	480
ACATGGCCAA ACAGGCCTTT GAGGAAGCCA TAGCTGAGCT TGACACTCTG GGAGAAGAAT	540
CCTACAAAGA CAGCACTCTC ATAATGCAGT TGCTGA	576

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

(B) CLONE: 4B11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ala Ala Thr Leu Gly Arg Asp Gln Tyr Val Tyr Met Ala Lys Leu
1 5 10 15

Ala Glu Gln Ala Glu Arg Tyr Glu Glu Met Val Gln Phe Met Glu Gln
20 25 30

Leu Val Thr Gly Ala Thr Pro Ala Glu Glu Leu Thr Val Glu Glu Arg
35 40 45

Asn Leu Leu Ser Val Ala Tyr Lys Asn Val Ile Gly Ser Leu Arg Ala
50 55 60

Ala Trp Arg Ile Val Ser Ser Ile Glu Gln Lys Glu Glu Ser Arg Lys
65 70 75 80

Asn Asp Glu His Val Ser Leu Val Lys Asp Tyr Arg Ser Lys Val Glu
85 90 95

Ser Glu Leu Ser Ser Val Cys Ser Gly Ile Leu Lys Leu Leu Asp Ser
100 105 110

His Leu Ile Pro Ser Ala Gly Ala Ser Glu Ser Lys Val Phe Tyr Leu
115 120 125

Lys Met Lys Gly Asp Tyr His Arg Tyr Met Ala Glu Phe Lys Ser Gly
130 135 140

Asp Glu Arg Lys Thr Ala Ala Glu Asp Thr Met Leu Ala Tyr Lys Ala
145 150 155 160

Ala Gln Asp Ile Ala Ala Ala Asp Met Ala Pro Thr His Pro Ile Arg
165 170 175

Leu Gly Leu Ala Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn
180 185 190

Ser Ser Asp Lys Ala Cys Asn Met Ala Lys Gln Ala Phe Glu Glu Ala
195 200 205

Ile Ala Glu Leu Asp Thr Leu Gly Glu Glu Ser Tyr Lys Asp Ser Thr
210 215 220

Leu Ile Met Gln Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp
225 230 235 240

Met Gln Glu Gln Met Asp Glu Ala
245

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 659 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CGCCGCCACC GCGATGTACG TGATCTACCA CCCTCGTCGG CGTCGTTCT CCGTCCCCGTC	60
AATAAGAACG AGCCGCGTGA ACCTAACAAAC CTCCCTGTAT TCCTCCGTCT CTCATCTCTC	120
TTCCTTCITC AACTTCACTC TAATCTCAGA GAATCCAAAC CAACACCTCT CTTTCTCTTA	180
CGATCCTTTC ACCGTCACCG TTAATTCAAGC TAAATCCGGT ACGATGCTCG GTAACGGAAC	240
TGTTCCCTGCT TTCTTCAGCG ATAACGGTAA CAAAACITCG TTTCACGGCG TGATCGCTAC	300
GTCTACAGCG GCGCGTGAGT TAGATCCGGA TGAAGCTAAG CATCTGAGAT CAGATCTGAC	360
GCGCGCGCGT GTAGGATATG AGATCGAGAT GAGAACTAAA GTGAAGATGA TAATGGGAA	420
GCTGAAGAGT GAAGGAGTAG AGATCAAAGT GACATGTTGA AGGATTTGAA GGAACATATAC	480
CAAAAGGTAA AACTCCAATT GTAGCTACTT CTAAAAAAAC TAAGTGTAAAG TCTGATCTTA	540
GTGTCAAGTC TGGAAATGGA TTTCTAAAGG AATTGATAA TTTCACATTG AAATTCTATA	600
TATCTCTCTT TTCTCTGGT TTTGTGAAAC TTTGGATGAT CAAAGAATTG TTCATTGTC	659

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Arg	Ile	Cys	Cys	Cys	Phe	Trp	Ser	Ile	Leu	Ile	Ile	Leu	Ile	Leu
1								10						

5								15						
---	--	--	--	--	--	--	--	----	--	--	--	--	--	--

Ala	Leu	Met	Thr	Ala	Ile	Ala	Ala	Thr	Ala	Met	Tyr	Val	Ile	Tyr	His
20								25					30		

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Pro	Arg	Pro	Pro	Ser	Phe	Ser	Val	Pro	Ser	Ile	Arg	Ile	Ser	Arg	Val
35								40				45			

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Asn	Leu	Thr	Thr	Ser	Ser	Asp	Ser	Ser	Val	Ser	His	Leu	Ser	Ser	Phe
50								55			60				

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Phe	Asn	Phe	Thr	Leu	Ile	Ser	Glu	Asn	Pro	Asn	Gln	His	Leu	Ser	Phe
65								70			75		80		

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Ser	Tyr	Asp	Pro	Phe	Thr	Val	Thr	Val	Asn	Ser	Ala	Lys	Ser	Gly	Thr
85								90				95			

Met	Leu	Gly	Asn	Gly	Thr	Val	Pro	Ala	Phe	Phe	Ser	Asp	Asn	Gly	Asn
100								105				110			

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Lys	Thr	Ser	Phe	His	Gly	Val	Ile	Ala	Thr	Ser	Thr	Ala	Ala	Arg	Glu
115								120				125			

--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--

Leu	Asp	Pro	Asp	Glu	Ala	Lys	His	Leu	Arg	Ser	Asp	Leu	Thr	Arg	Ala
130								135			140				

Arg Val Gly Tyr Glu Ile Glu Met Arg Thr Lys Val Lys Met Ile Met
 145 150 155 160

Gly Lys Leu Lys Ser Glu Gly Val Glu Ile Lys Val Thr Cys
 165 170

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 3B76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCTCCAACTC CAGGCCAGCC AACAAAAGAA CCTACATTTA TTCCAGTGGT TGTGGTCTT	60
TTGGACTCAA GTGGGAAAGA CATTACTCTT TCCTCTGTC ATTATGATGG TACAGTGCAG	120
ACCATTCAG GCAGCAGCAC AATACTCGA GTGACAAGAA ACAAGAAGAG TTTGTGTTT	180
CTGATATAACC AGAAAGACCT GTCCGTCCC TATTTAGGGG ATTCAGCCCC AGITCGTGT	240
GAAACTGATC TCTCTAATGA TGACTTATTTC TTCCCTCTAG CACATGATTC AGATGAATT	300
AATAGGTGGG AGGCCGGTCA AGITCTGGCA AGAAAGCTGA TGCTGAACCT AGITTCGTGAT	360
TTCCAGCAAA ATAAACCGTT GGCTCTAAAC CCAAAATTG TGCAAGGTCT CGGCAGTGTG	420
CTTTCTGACT CAAGCTTGGA CAAGGAATTG ATAGCCAAAG CAATAACACT ACCTGGGGAG	480
GGAGAGATAA TGGACATGAT GGCGTGGCG GATCCTGATG CTGTCATGC TGTAGAAAG	540
TTTGTACGAA AGCAGCTTGC ATCTGAACCT AAGGAGGAGC TTCT	584

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Arabidopsis thaliana

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 3B76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Pro	Pro	Thr	Pro	Gly	Gln	Pro	Thr	Lys	Glu	Pro	Thr	Phe	Ile	Pro	Val
1															15

Val	Val	Gly	Leu	Leu	Asp	Ser	Ser	Gly	Lys	Asp	Ile	Thr	Leu	Ser	Ser
															30
20															

Val	His	Tyr	Asp	Gly	Thr	Val	Gln	Thr	Ile	Thr	Gly	Ser	Ser	Thr	Ile
															45
35															

Leu	Arg	Val	Thr	Lys	Lys	Gln	Glu	Glu	Phe	Val	Phe	Ser	Asp	Ile	Pro
															60
50															

Glu	Arg	Pro	Val	Pro	Ser	Leu	Phe	Arg	Gly	Phe	Ser	Ala	Pro	Val	Arg
															80
65															

Val	Glu	Thr	Asp	Leu	Ser	Asn	Asp	Leu	Phe	Phe	Leu	Leu	Ala	His
85														95

Asp	Ser	Asp	Glu	Phe	Asn	Arg	Trp	Glu	Ala	Gly	Gln	Val	Leu	Ala	Arg
															110
100															

Lys	Leu	Met	Leu	Asn	Leu	Val	Ser	Asp	Phe	Gln	Gln	Asn	Lys	Pro	Leu
															125
115															

Ala	Leu	Asn	Pro	Lys	Phe	Val	Gln	Gly	Leu	Gly	Ser	Val	Leu	Ser	Asp
															140
130															

Ser Ser Leu Asp Lys Glu Phe Ile Ala Lys Ala Ile Thr Leu Pro Gly
 145 150 155 160
 Glu Gly Glu Ile Met Asp Met Met Ala Val Ala Asp Pro Asp Ala Val
 165 170 175
 His Ala Val Arg Lys Phe Val Arg Lys Gln Leu Ala Ser Glu Leu Lys
 180 185 190
 Glu Glu Leu Lys Ile Val Glu Asn Asn Arg Ser Thr Glu Ala Tyr Val
 195 200 205
 Phe Asp His Ser Asn Met Ala Arg Arg Ala Leu Lys Asn Thr Ala Leu
 210 215 220
 Ala Tyr Leu Ala Ser Leu Glu Asp Pro Ala Tyr Met Gly Thr Cys Thr
 225 230 235 240
 Glu Arg Ile Gln Gly Gly His Gln Phe Asp Arg Pro Ile Cys Cys Phe
 245 250 255
 Gly Thr Leu Ser Gln Asn Pro Gly Lys Thr Arg Glu Arg Thr Phe Leu
 260 265 270
 Pro Asp Phe Tyr Glu Gln Val Ala Gly Thr Ile
 275 280

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Arabidopsis thaliana
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: 4A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACCAGGAGGG GAAAAAGTCT TACCCCATGG ACATCCCGGG GATTGAGTGT TACCCGAAAA	60
GGATGAAGAA TGGTATTCCCT CCGTCGTGGA CCCCATGCAC CCATTGGGAA AGCCGTGTGG	120
CGTTTTCTTT CAGGGATGAT AGAAAAGTGC TCCCTGGGA TGGAAAGGAG GAGCCTTTAC	180
TGGTAGTGGC CGATAGGGTG AGGAATGTIG TGGAGGCTGA TGACGGGTAT TATCTCGTGG	240
TGGCTGAGAA CGGACTTAAG CTAGAGAAAG GATCAGATTT GAAGGCGAGA GAGGTGAAGG	300
AGAGTTTACG GATGGTTGTT TTGGGGTGA GGCGCCAAG AGAAGATGAT GATGATTGGC	360
AGACAAGTCA TCAGAACTGG GACTGAATTAA ATAGAACCAA TACTCATATG CTGTAACGTGA	420
TTACGGAGTC ATCATGGTCA TGTAAAATT TTGGATAAAAG GTGGTAACCT TTGTTCTAA	480
GATACAATCA GAAACAGAGC AATATTTTC TCTAAAAAAA AAAAAAAA AAAA	534

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Arabidopsis thaliana*

(vii) IMMEDIATE SOURCE:

- (B) CLONE: 4A5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asp Ile Pro Gly Ile Glu Cys Tyr Pro Lys Arg Met Lys Asn Gly			
1	5	10	15
Ile Pro Pro Ser Trp Thr Pro Cys Thr His Trp Glu Ser Arg Val Ala			
20	25	30	

Phe Ser Phe Arg Asp Asp Arg Lys Val Leu Pro Trp Asp Gly Lys Glu
 35 40 45

Glu Pro Leu Leu Val Val Ala Asp Arg Val Arg Asn Val Val Glu Ala
 50 55 60

Asp Asp Gly Tyr Tyr Leu Val Val Ala Glu Asn Gly Leu Lys Leu Glu
 65 70 75 80

Lys Gly Ser Asp Leu Lys Ala Arg Glu Val Lys Glu Ser Leu Gly Met
 85 90 95

Val Val Leu Val Val Arg Pro Pro Arg Glu Asp Asp Asp Asp Trp Gln
 100 105 110

Thr Ser His Gln Asn Trp Asp
 115

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer V6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGCTTTGCA TAACTTTGAG G

21

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer T7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AATACGGACTC ACTATAG

17